

Query Match Similarity 99.7%; Score 2704; DB 2; Length 517;  
Best Local Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MSRSRDKTEQQSOTSSSSRAPOSTQSOSSTSLSDPVPVODASLSPEDPBDID 60  
1 MSRSRDKTEQQSOTSSSSAPOSTQSOSSTSLSDPVPVODASLPEDPBDID 60

61 IPOPQKRLMALKGKPLNHDCLHRYVFRDCKCDYTRIPMANOTRYKTSKRHRIFO 120  
61 IPOPQKRLMALKGKPLNHDCLHRYVFRDCKCDYTRIPMANOTRYKTSKRHRIFO 120

61 IPOPQKRLMALKGKPLNHDCLHRYVFRDCKCDYTRIPMANOTRYKTSKRHRIFO 120  
61 IPOPQKRLMALKGKPLNHDCLHRYVFRDCKCDYTRIPMANOTRYKTSKRHRIFO 120

121 ELGHGHGSRVANIEEDISGNGTTFVNKEIGKERTPLTNNAEIALSLPTNKVTPVPSVDD 180  
121 ELGHGHGSRVANIEEDISGNGTTFVNKEIGKERTPLTNNAEIALSLPTNKVTPVPSVDD 180

181 QTYPKDPIKYMSPAPGSGCAGCGEVKLAPOSKVCKAVKCKRKPMNTSSNEHPI 240  
181 QTYPKDPIKYMSPAPGSGCAGCGEVKLAPOSKVCKAVKCKRKPMNTSSNEHPI 240

241 VDTETBLKQDHPCTIKENPPDSEFTYVILMEGELDFDRVNSTRBPAKLYF 300  
241 VDTETBLKQDHPCTIKENPPDSEFTYVILMEGELDFDRVNSTRBPAKLYF 300

301 YOMLAVOYIHENGVHRDLKPENVLSTSSECCIKTDPSOKLGETSMRTGTP 360  
301 YOMLAVOYIHENGVHRDLKPENVLSTSSECCIKTDPSOKLGETSMRTGTP 360

361 TYLAPKVNTAGTGYSAVCWSLGVILFVLCGYPPESONTFLKQDAEGKTYI 420  
361 TYLAPKVNTAGTGYSAVCWSLGVILFVLCGYPPESONTFLKQDAEGKTYI 420

361 TTYLAPKVNTAGTGYSAVCWSLGVILFVLCGYPPESONTFLKQDAEGKTYI 420  
361 TTYLAPKVNTAGTGYSAVCWSLGVILFVLCGYPPESONTFLKQDAEGKTYI 420

421 AAJAWRVSBEQDPLVNLVDPORLTQALEHPWQDSKMRHTVERLMGVDTMP 480  
421 AAJAWRVSBEQDPLVNLVDPORLTQALEHPWQDSKMRHTVERLMGVDTMP 480

481 PIKKNIKRGHEDODASTSSCSEBILPTSAEGRAKR 517  
481 PIKKNIKRGHEDODASTSSCSEBILPTSAEGRAKR 517

481 PIKKNIKRGHEDODASTSSCSEBILPTSAEGRAKR 517  
481 PIKKNIKRGHEDODASTSSCSEBILPTSAEGRAKR 517

**RESULT 2**

OBSTWO PRELIMINARY; PRT; S17 AA.

ID OBSTWO  
AC OBSTWO  
DT 01-JUN-2001 (TRIMBLE, 17, Created)  
DT 01-OCT-2003 (TRIMBLE, 25, Last annotation update)  
DT Protein kinase Cdb1.  
GN Name=Cdb1;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopidae; Xenopus.  
RN NCBI\_TaxId=8155;  
RN SEQUENCE FROM N.A.  
RA Matsui T., Nakamichi M., Takizawa H.,  
RL Submitted (DRC-000) to the SWISS/GenBank/DBJ databases.  
RN - SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
RN EMBL: AF326574; AAGG59841; -.  
RN HSP: 096107, IGC.C.  
RN GO: GO:000524: P:ARP binding; IBA.  
RN GO: GO:000674: P:protein serine/threonine kinase activity; IER.  
RN GO: GO:0016740: P:transpherase activity; IER.  
RN GO: GO:006668: P:protein amino acid phosphorylation; IER.  
RN InterPro: IPR000453: PHA.  
RN InterPro: IPR1100: Kinase like.  
RN InterPro: IPR000719: Prot Kinase.  
RN InterPro: IPR002290: Ser Thr kinase.  
RN InterPro: IPR00271: Ser-Thr protein AS.  
RN InterPro: IPR00984: SMA5\_PHA.  
RN PFM: PFO0598; FRA: 1.  
RN PFM: PFO0099; Pfimate; 1.  
RN ProDom; PDom0001; Prot\_kinase; 1.  
RN SMART; SM00240; PFA; 1.  
RN SMART; SM00220; S\_TKC\_1.  
RN PROSITE; PS00016; PROTEIN\_KINASE\_DOMAIN; 1.  
RN PROSITE; PS000108; PROTEIN\_KINASE\_ST; 1.  
RN ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
RN SCOURNCB; 517 AA; -58310 MM; 4013235AA0BDCBB CRC64;  
SQ

**RESULT 3**

CHK2\_HUMAN CHK2\_HUMAN STANDARD; PRT; S43 AA.

ID CHK2\_HUMAN  
AC 056017; Q9JKP0; Q9UQF1;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 23-OCT-2004 (Rel. 45, Last annotation update)

DE Serine/threonine-protein kinase Chk2 (EC 2.7.1.37) (Cds1).  
GN Name=CHK2, Synonyms=CHK2,  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Gutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxId=9506;

[1] SEQUENCE FROM N.A. MEDLINE-99010819; PubMed=9883122; DOI=10.1016/S0960-9822(99)80041-4;  
RA Blasina A., van de Weyer I., Laus M.C., Luyten W.H.M.L., Parker A.E.,  
RA McCowan C.H.; "A human homologue of the checkpoint kinase Cdb1 directly inhibits  
RT Cdc25 phosphatase"; Curr. Biol. 9:1-10(1999).

RL [2] SEQUENCE FROM N.A. MEDLINE-99010819; PubMed=9883122; DOI=10.1016/S0960-9822(99)80041-4;  
RX RA Matsushita S., Huang M., Rilleme S.J.; "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase." Science 282:1893-1897(1998).  
RT [3] SEQUENCE FROM N.A. MEDLINE=9919255; PubMed=10027108; DOI=10.1073/pnas.96.7.3745; Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Pilnicka-Worms H.,



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CC	Q9R019	PRELIMINARY,	PRT:	545 AA.
CC	Q9R019;			
DR	01-MAY-2000 (T-EMBL; 13' Created)			
DR	01-MAY-2000 (T-EMBL; 13; Last sequence update)			
DT	01-OCT-2003 (T-EMBL; 25; Last annotation update)			
DB	Checkpoint kinase Chk2.			
OS	Rattus norvegicus (Rat).			
OC	Bukarrotta; Metazoa; Chordata; Craniate; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OK	Ncbi_TaxId:10116;			
RN	[1]			
RP	SEQUENCE FROM N.I.A.			
RC	TISSUE:thymus;			
TX	Medline:9361938; PubMed:10415585; DOI:10.1038/sj.onc.1202925;			
RA	Chaturvedi P., Eng W.K., Zhu Y., Matern M.R., Misra R., Harle M.R.,			
RA	Zhang X., Annan R.S., Lu Q., Fauchette L.P., Scott G.F., Li X.,			
RA	Corr S.A., Johnson R.K., Winkler J.D., Zhou B.B.;			
RT	"Mammalian Chk2 is a downstream effector of the ATM-dependent DNA			
RT	damage checkpoint pathway.";			
RL	Oncogene 18:4047-4054(1999).			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL: AP134054; AA055890.1; -.			
DR	HSSP; Q96017; IGCX.			
DR	GO; GO:000534; C:nucleus, NAS.			
DR	GO; GO:004674; P:protein serine/threonine kinase activity; TAS.			
DR	GO; GO:000077; P:DNA damage response, signal transduction; ze. . ; TAS.			
DR	InterPro: IPR000253; PHA.			
DR	InterPro: IPR01009; Kinase like.			
DR	InterPro: IPR000719; Prot_kinase.			
Query Match	Best Local Similarity 61.0%; Score 1655.5; DB 1; Length 543;			
DR	Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;			
Qy	2 MSRDKTKEQSQQ-----OSQGSSSSSAP-QSSQSSSSGT 37			
Db	1 NSRSRDSVQAQSRGHGSSACSOHGSVYQSQGSSSSGSSSTMMNSCOSHSSGTL 60			
Qy	38 SSQDVTVPDQASI----PDPDPRDOPQPKWMLKGSLKNDCLHHEVYFGDKK 92			
Db	61 SSQDVTVPDQASIPDOPBEPBEPBPAPWMLWALQDGFPANLCEVNNTWFGDKK 120			
Qy	93 CQTPDPVQVQMDRTKTYSPHRPPIQLGHSRVRVNTISLGNGQTPKVIGKRT 152			
Db	121 CBYCFDPEPLKTKDQKTYSPHKFRFVSGPKSYVIBDNGNTFVTFVBLGKGR 180			
Qy	153 LPETNKAIALSLPTKVKYFDSQDSDVDTIYRDPKXINHSPGCGACEVLAQK 212			
Db	161 RPANNNSKIAISLSRKVYFVFDLTDOSVYKAKRDIYHISTLGSAGCIVLAQF 240			
Qy	213 SYVKKVAKVAKTSKRRKPTNSNEHP-LSVTEHLIKLDPCKIKKANTPSDFYI 271			
Db	241 KTCCKVAKVAKTSKRRKPAIGAREADPALKVTEBILQKHNHCICKNKFDD-A-YI 299			
Qy	272 VLRALMGGGRDVRVNSTRLAPIVQLYTOMLAVQVHLHENGVIRDLKPKAVLSTS 331			
Db	300 VLRALMGGGRDVRVNSTRLAPIVQLYTOMLAVQVHLHENGVIRDLKPKAVLSTS 359			
Qy	332 RSCCKITDPEQSKLIGTSMLRTQGTTPTVLPREVNTAGTAGYSSAVDWLQVLFV 391			
Db	360 RSCCKITDPEQSKLIGTSMLRTQGTTPTVLPREVNTAGTAGYSSAVDWLQVLFV 419			
Qy	392 CLGYPPEPSSESNPLKQIAEGKTYIAAMTVNSQAPLVNLVVDPEQITKO 451			
Db	420 CLGYPPEPSSENRVTSKQDQITSGKRNPIPEVWAEVSEKALDVLKGLVWDPKRPTT 479			
Qy	452 ALERPHWODPSMKTTERLVMGVDHMP---IKKNIKRGCHEWMDASTSS----C 503			
Db	480 ALERPHWODPSMKTTERLVMGVDHMP---IKKNIKRGCHEWMDASTSS----C 539			
Qy	504 SRL 507			
Db	540 AAVL 543			

RESULT 4  
Q9R019

296 AKLYFQMLAIVQVHLHENGVIRDLKPKAVLSTSBCCKITDQSKLIGTSMLRT 355

327 CKYFQMLAIVQVHLHENGVIRDLKPKAVLSTSBCCKITDQSKLIGTSMLRT 386

356 LGTPYTLAPREVNTAGTAGYSSAVDWLQVLFVCLGYPPEPSSESNPLKQIAE 415